

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/526,133
Source: IFWP
Date Processed by STIC: 08/07/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 08/07/2006

PATENT APPLICATION: US/10/526,133

TIME: 10:07:15

Input Set : A:\18612.seq.txt

Output Set: N:\CRF4\08072006\J526133.raw

3 <110> APPLICANT: Brugliera, Filippa
 4 Tanaka, Yoshikazu
 5 Mason, John
 7 <120> TITLE OF INVENTION: Flavonoid 3',5' Hydroxylase Gene Sequences and Uses Therefor
 9 <130> FILE REFERENCE: 18612
 11 <140> CURRENT APPLICATION NUMBER: 10/526,133
 12 <141> CURRENT FILING DATE: 2005-02-28
 14 <150> PRIOR APPLICATION NUMBER: AU 2002951088
 15 <151> PRIOR FILING DATE: 2002-08-30
 17 <160> NUMBER OF SEQ ID NOS: 32
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1812
 23 <212> TYPE: DNA
 24 <213> ORGANISM: petunia
 26 <400> SEQUENCE: 1

(Pg-6)

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33	taatcatttc	aactcttatt	tcaaaaacta	cgggccggca	tctaccgccg	gggccaagag	240
35	ggtggccggt	gacgagagca	cttccacttt	taggagccat	gccacatgtt	tccttagcta	300
37	aaatggcaaa	aaaatatgga	gcaatcatgt	atctcaaagt	tggaacatgt	ggcatggcag	360
39	ttgcttctac	ccctgatgct	gctaagcat	tcttgaaaac	acttgatata	aacttctcca	420
41	atcgctccacc	taatgcaggt	gccactcact	tagcttataa	tgctcaagac	atgggtttttg	480
43	cacattatgg	accacgatgg	aagttgctaa	ggaaattaag	caacttgcac	atgctagggg	540
45	gaaaagcctt	agagaattgg	gcaaatgttc	gtgccaatga	gctagggcac	atgctaaaat	600
47	caatgtccga	tatgagtcga	gagggccaga	gggttggtgtg	ggcggagatg	ttgacatttg	660
49	ccatggccaa	tatgatcgga	caagtgatgc	taagcaaaaag	agtattttgt	gataaagggtg	720
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57	caactaccta	tgaacgtaag	gggaaaccag	attttcttga	tggtgttatg	gaaaatgggg	960
59	acaattctga	aggagaaaga	ctcagtacaa	ccaacatcaa	agcacttttg	ctgaatttgt	1020
61	tcacagctgg	tacggacact	tcttctagtg	caatagaatg	ggcacttgca	gaaatgatga	1080
63	agaaccctgc	catttttga	aaagcacaa	cagaaatgga	tcaagtcatt	ggaagaaata	1140
65	ggcggtttact	cgaatccgat	atcccaaate	tcccttacct	ccgagcaatt	tgcaaagaaa	1200
67	catttcgaaa	acacccttct	acaccattaa	atcttcctag	gatctcgaac	gaaccatgca	1260
69	tagtcgatgg	ttattacata	ccaaaaaaca	ctaggcttag	tggttaacata	tgggcaattg	1320
71	gaagagatcc	ccaagtttgg	gaaaatccac	tagagtttaa	tcccgaagaa	ttcttgagtg	1380
73	gaagaaactc	caagattgat	cctcgagggg	acgattttga	attgatacca	tttggtgctg	1440
75	gacgaagaat	ttgtgcagga	acaagaatgg	gaattgta	ggtggaatat	atattaggaa	1500
77	ctttggttca	ttcatttgat	tggaaattac	caagtgaagt	tattgagttg	aatatggaag	1560
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83 tgttggttgt agcatgagat attaaaagga gtacatgaag cgcattgcat gagtttaact 1740
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92 <212> TYPE: PRT
93 <213> ORGANISM: petunia
95 <400> SEQUENCE: 2
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102 20 25 30
105 Leu Pro Pro Gly Pro Arg Gly Trp Pro Val Ile Gly Ala Leu Pro Leu
106 35 40 45
109 Leu Gly Ala Met Pro His Val Ser Leu Ala Lys Met Ala Lys Lys Tyr
110 50 55 60
113 Gly Ala Ile Met Tyr Leu Lys Val Gly Thr Cys Gly Met Ala Val Ala
114 65 70 75 80
117 Ser Thr Pro Asp Ala Ala Lys Ala Phe Leu Lys Thr Leu Asp Ile Asn
118 85 90 95
121 Phe Ser Asn Arg Pro Pro Asn Ala Gly Ala Thr His Leu Ala Tyr Asn
122 100 105 110
125 Ala Gln Asp Met Val Phe Ala His Tyr Gly Pro Arg Trp Lys Leu Leu
126 115 120 125
129 Arg Lys Leu Ser Asn Leu His Met Leu Gly Gly Lys Ala Leu Glu Asn
130 130 135 140
133 Trp Ala Asn Val Arg Ala Asn Glu Leu Gly His Met Leu Lys Ser Met
134 145 150 155 160
137 Ser Asp Met Ser Arg Glu Gly Gln Arg Val Val Val Ala Glu Met Leu
138 165 170 175
141 Thr Phe Ala Met Ala Asn Met Ile Gly Gln Val Met Leu Ser Lys Arg
142 180 185 190
145 Val Phe Val Asp Lys Gly Val Glu Val Asn Glu Phe Lys Asp Met Val
146 195 200 205
149 Val Glu Leu Met Thr Ile Ala Gly Tyr Phe Asn Ile Gly Asp Phe Ile
150 210 215 220
153 Pro Cys Leu Ala Trp Met Asp Leu Gln Gly Ile Glu Lys Arg Met Lys
154 225 230 235 240
158 Arg Leu His Lys Lys Phe Asp Ala Leu Leu Thr Lys Met Phe Asp Glu
159 245 250 255
162 His Lys Ala Thr Thr Tyr Glu Arg Lys Gly Lys Pro Asp Phe Leu Asp
163 260 265 270
166 Val Val Met Glu Asn Gly Asp Asn Ser Glu Gly Glu Arg Leu Ser Thr
167 275 280 285
170 Thr Asn Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp
171 290 295 300
174 Thr Ser Ser Ser Ala Ile Glu Trp Ala Leu Ala Glu Met Met Lys Asn
175 305 310 315 320

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182 Arg Asn Arg Arg Leu Leu Glu Ser Asp Ile Pro Asn Leu Pro Tyr Leu
183           340           345           350
186 Arg Ala Ile Cys Lys Glu Thr Phe Arg Lys His Pro Ser Thr Pro Leu
187           355           360           365
190 Asn Leu Pro Arg Ile Ser Asn Glu Pro Cys Ile Val Asp Gly Tyr Tyr
191           370           375           380
194 Ile Pro Lys Asn Thr Arg Leu Ser Val Asn Ile Trp Ala Ile Gly Arg
195 385           390           395           400
198 Asp Pro Gln Val Trp Glu Asn Pro Leu Glu Phe Asn Pro Glu Arg Phe
199           405           410           415
202 Leu Ser Gly Arg Asn Ser Lys Ile Asp Pro Arg Gly Asn Asp Phe Glu
203           420           425           430
206 Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Thr Arg Met
207           435           440           445
210 Gly Ile Val Met Val Glu Tyr Ile Leu Gly Thr Leu Val His Ser Phe
211           450           455           460
215 Asp Trp Lys Leu Pro Ser Glu Val Ile Glu Leu Asn Met Glu Glu Ala
216 465           470           475           480
219 Phe Gly Leu Ala Leu Gln Lys Ala Val Pro Leu Glu Ala Met Val Thr
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227 <210> SEQ ID NO: 3

228 <211> LENGTH: 1756

229 <212> TYPE: DNA

230 <213> ORGANISM: petunia

232 <400> SEQUENCE: 3

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237 ggcgtctccc gccagggcca agaggggtggc cgggtgatcgg agcacttcca cttttaggag      180
239 ccatgccaca tgtttcctta gctaaaatgg caaaaaaata tggagcaatc atgtatctca      240
241 aagttggaac gtgtggcatg gtagttgctt ctaccctga tgctgctaaa gcgttcttga      300
243 aaacacttga tctcaacttc tccaatcgtc cacctaatgc aggtgccacc cacttagcct      360
245 atggtgctca agacatgggt tttgcacatt atggaccaag atggaagttg ctaaggaaat      420
247 taagcaactt acatatgcta ggggggaaag ctttagaaaa ttgggcaaat gttcgtgcca      480
249 atgagctagg acacatgcta aaatcgatgt ttgatatgag cagagaaggg gagagagttg      540
251 tgggtggcgga gatgttgaca tttgccatgg cgaatatgat cggacaggtg atacttagca      600
253 aaagagtatt tgtaataaaa ggtgttgagg taaatgaatt taaggacatg gtggtagagt      660
255 taatgacaac agcaggggat tttaacattg gtgattttat tccttgttta gcttggatgg      720
257 atttacaagg gatagaaaaa ggaatgaaac gtttacataa gaagtttgat gctttattga      780
259 caaagatggt tgatgaacac aaagcaacta gctatgaacg taaggggaaa ccagattttc      840
261 ttgatttgtg tatggaaaat agggacaatt ctgaaggaga aaggctcagt acaaccaaca      900
263 tcaaagcact cttgctgaat ttgttcacag ctggtacaga cacttcttct agtgcaatag      960
265 aatgggcact tgcagagatg atgaagaacc ctgccatttt aaagaaagca caaggagaaa     1020
267 tggatcaagt cattggaaac aataggcgtc tgctcgaatc ggatatccca aatctccctt     1080
269 acctccgagc aatttgcaaa gaaacatttc gaaagcacc ttctacacca ttaaattctcc     1140
271 ctaggatctc gaacgaacca tgcattgtcg atggttatta catacaaaaa aacactaggc     1200

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273 ttagtggttaa catatgggca attggaagag atcccgaagt ttgggagaac ccactagagt 1260
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277 ttgaattgat accatttggg gctggacgaa gaatttgtgc agggacaaga atgggaatcg 1380
279 taatggtgga atatatatta ggaactttgg tccattcatt tgattggaaa ttaccaagtg 1440
281 aagttattga gctaaatatg gaagaagctt ttggattagc tttgcagaaa gctgtccctc 1500
283 ttgaagctat ggttactcca aggctgccta ttgatgttta tgcaccttta gcttgaaaca 1560
285 tgcctttacg ttgggtttcag ttttgggtag tataatgttg tgggtgttgg ctatagaaat 1620
287 attaataaat gctagtatct tgaaggcgcg tgcaggggga gggggttgtc ttagatagta 1680
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295 <211> LENGTH: 508
296 <212> TYPE: PRT
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306 20 25 30
309 Leu Pro Pro Gly Pro Arg Gly Trp Pro Val Ile Gly Ala Leu Pro Leu
310 35 40 45
313 Leu Gly Ala Met Pro His Val Ser Leu Ala Lys Met Ala Lys Lys Tyr
314 50 55 60
317 Gly Ala Ile Met Tyr Leu Lys Val Gly Thr Cys Gly Met Val Val Ala
318 65 70 75 80
321 Ser Thr Pro Asp Ala Ala Lys Ala Phe Leu Lys Thr Leu Asp Leu Asn
322 85 90 95
325 Phe Ser Asn Arg Pro Pro Asn Ala Gly Ala Thr His Leu Ala Tyr Gly
326 100 105 110
329 Ala Gln Asp Met Val Phe Ala His Tyr Gly Pro Arg Trp Lys Leu Leu
330 115 120 125
333 Arg Lys Leu Ser Asn Leu His Met Leu Gly Gly Lys Ala Leu Glu Asn
334 130 135 140
337 Trp Ala Asn Val Arg Ala Asn Glu Leu Gly His Met Leu Lys Ser Met
338 145 150 155 160
341 Phe Asp Met Ser Arg Glu Gly Glu Arg Val Val Val Ala Glu Met Leu
342 165 170 175
345 Thr Phe Ala Met Ala Asn Met Ile Gly Gln Val Ile Leu Ser Lys Arg
346 180 185 190
349 Val Phe Val Asn Lys Gly Val Glu Val Asn Glu Phe Lys Asp Met Val
350 195 200 205
353 Val Glu Leu Met Thr Thr Ala Gly Tyr Phe Asn Ile Gly Asp Phe Ile
354 210 215 220
357 Pro Cys Leu Ala Trp Met Asp Leu Gln Gly Ile Glu Lys Gly Met Lys
358 225 230 235 240
361 Arg Leu His Lys Lys Phe Asp Ala Leu Leu Thr Lys Met Phe Asp Glu
362 245 250 255
365 His Lys Ala Thr Ser Tyr Glu Arg Lys Gly Lys Pro Asp Phe Leu Asp
366 260 265 270

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RAW SEQUENCE LISTING

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Input Set : A:\18612.seq.txt

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377 Thr Ser Ser Ser Ala Ile Glu Trp Ala Leu Ala Glu Met Met Lys Asn
378 305      310      315      320
381 Pro Ala Ile Leu Lys Lys Ala Gln Gly Glu Met Asp Gln Val Ile Gly
382      325      330      335
386 Asn Asn Arg Arg Leu Leu Glu Ser Asp Ile Pro Asn Leu Pro Tyr Leu
387      340      345      350
390 Arg Ala Ile Cys Lys Glu Thr Phe Arg Lys His Pro Ser Thr Pro Leu
391      355      360      365
394 Asn Leu Pro Arg Ile Ser Asn Glu Pro Cys Ile Val Asp Gly Tyr Tyr
395      370      375      380
398 Ile Pro Lys Asn Thr Arg Leu Ser Val Asn Ile Trp Ala Ile Gly Arg
399 385      390      395      400
402 Asp Pro Glu Val Trp Glu Asn Pro Leu Glu Phe Tyr Pro Glu Arg Phe
403      405      410      415
406 Leu Ser Gly Arg Asn Ser Lys Ile Asp Pro Arg Gly Asn Asp Phe Glu
407      420      425      430
410 Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Thr Arg Met
411      435      440      445
414 Gly Ile Val Met Val Glu Tyr Ile Leu Gly Thr Leu Val His Ser Phe
415      450      455      460
418 Asp Trp Lys Leu Pro Ser Glu Val Ile Glu Leu Asn Met Glu Glu Ala
419 465      470      475      480
422 Phe Gly Leu Ala Leu Gln Lys Ala Val Pro Leu Glu Ala Met Val Thr
423      485      490      495
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427      500      505
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431 <211> LENGTH: 2934
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433 <213> ORGANISM: rosa
435 <400> SEQUENCE: 5
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440 aggagaatgt tgaaagatct aatgatgagc actctgttaa actagacgga attcatgtgc      180
442 agcacgagtg tcatgagggc agtgaagaag acaaacctga tggtaagagc ggtgagaatg      240
444 cagttgatct ggctaatacat ggcattggctc gaactgattt ttgtcagata acagaagaga      300
446 ttgagaatgg agtagtcatc actgagatga gcaacattgc caaccctgat aaaactgata      360
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450 ctaatacaaaa ggaagtgaca gaagagaatt ctgacagacg tgcgaaggaa gtgacagaag      480
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460 atcgggagcc ggttggtcct actcctgatg gtaatttttc tgtggatatg gattactata      780
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/526,133

DATE: 08/07/2006
TIME: 10:07:16

Input Set : A:\18612.seq.txt
Output Set: N:\CRF4\08072006\J526133.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; N Pos. 307
Seq#:17; N Pos. 1372
Seq#:30; N Pos. 2051

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/526,133

DATE: 08/07/2006

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Input Set : A:\18612.seq.txt

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L:782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:300
L:1427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:1320
L:2592 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:2040